



- 1 -

SEQUENCE LISTING

<110> Luecke, Hartmut
Prosise, Glen

<120> Crystal Structures of T. Foetus Inosine
Monophosphate Dehydrogenase In Complex With Substrate,
CoFactor and Analogs and Uses Thereof

<130> 66778-355

<140> US 10/663,347
<141> 2003-09-15

<150> 60/410,523
<151> 2002-09-13

<150> 60/412,044
<151> 2002-09-18

<160> 2

<170> FastSEQ for Windows Version 4.0

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<211> 503
<212> PRT
<213> Tritrichomonas foetus

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Leu Ile Pro Gly Leu Ser Thr Val Asp Cys Ile Pro Ser Asn Val Asn
20 25 30
Leu Ser Thr Pro Leu Val Lys Phe Gln Lys Gly Gln Ser Glu Ile
35 40 45
Asn Leu Lys Ile Pro Leu Val Ser Ala Ile Met Gln Ser Val Ser Gly
50 55 60
Glu Lys Met Ala Ile Ala Leu Ala Arg Glu Gly Gly Ile Ser Phe Ile
65 70 75 80
Phe Gly Ser Gln Ser Ile Glu Ser Gln Ala Ala Met Val His Ala Val
85 90 95
Lys Asn Phe Lys Ala Gly Phe Val Val Ser Asp Ser Asn Val Lys Pro
100 105 110
Asp Gln Thr Phe Ala Asp Val Leu Ala Ile Ser Gln Arg Thr Thr His
115 120 125
Asn Thr Val Ala Val Thr Asp Asp Gly Thr Pro His Gly Val Leu Leu
130 135 140
Gly Leu Val Thr Gln Arg Asp Tyr Pro Ile Asp Leu Thr Gln Thr Glu
145 150 155 160
Thr Lys Val Ser Asp Met Met Thr Pro Phe Ser Lys Leu Val Thr Ala

	165	170	175
His Gln Asp Thr Lys Leu Ser Glu Ala Asn Lys Ile Ile Trp Glu Lys			
180	185	190	
Lys Leu Asn Ala Leu Pro Ile Ile Asp Asp Asp Gln His Leu Arg Tyr			
195	200	205	
Ile Val Phe Arg Lys Asp Tyr Asp Arg Ser Gln Val Cys His Asn Glu			
210	215	220	
Leu Val Asp Ser Gln Lys Arg Tyr Leu Val Gly Ala Gly Ile Asn Thr			
225	230	235	240
Arg Asp Phe Arg Glu Arg Val Pro Ala Leu Val Glu Ala Gly Ala Asp			
245	250	255	
Val Leu Cys Ile Asp Ser Ser Asp Gly Phe Ser Glu Trp Gln Lys Ile			
260	265	270	
Thr Ile Gly Trp Ile Arg Glu Lys Tyr Gly Asp Lys Val Lys Val Gly			
275	280	285	
Ala Gly Asn Ile Val Asp Gly Glu Gly Phe Arg Tyr Leu Ala Asp Ala			
290	295	300	
Gly Ala Asp Phe Ile Lys Ile Gly Ile Gly Gly Ser Ile Cys Ile			
305	310	315	320
Thr Arg Glu Gln Lys Gly Ile Gly Arg Gly Gln Ala Thr Ala Val Ile			
325	330	335	
Asp Val Val Ala Glu Arg Asn Lys Tyr Phe Glu Glu Thr Gly Ile Tyr			
340	345	350	
Ile Pro Val Cys Ser Asp Gly Gly Ile Val Tyr Asp Tyr His Met Thr			
355	360	365	
Leu Ala Leu Ala Met Gly Ala Asp Phe Ile Met Leu Gly Arg Tyr Phe			
370	375	380	
Ala Arg Phe Glu Glu Ser Pro Thr Arg Lys Val Thr Ile Asn Gly Ser			
385	390	395	400
Val Met Lys Glu Tyr Trp Gly Glu Gly Ser Ser Arg Ala Arg Asn Trp			
405	410	415	
Gln Arg Tyr Asp Leu Gly Gly Lys Gln Lys Leu Ser Phe Glu Glu Gly			
420	425	430	
Val Asp Ser Tyr Val Pro Tyr Ala Gly Lys Leu Lys Asp Asn Val Glu			
435	440	445	
Ala Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu			
450	455	460	
Thr Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser			
465	470	475	480
Val Ser Ile Val Glu Gly Ala His Asp Val Ile Val Lys Asp Arg			
485	490	495	
Ile Asn Asp Tyr His Pro Lys			
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<212> PRT
<213> Tritrichomonas foetus

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<223> Xaa = S-Hydroxycysteine

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Met Ala Lys Tyr Tyr Asn Glu Pro Cys His Thr Phe Asn Glu Tyr Leu
1 5 10 15
Leu Ile Pro Gly Leu Ser Thr Val Asp Cys Ile Pro Ser Asn Val Asn
20 25 30
Leu Ser Thr Pro Leu Val Lys Phe Gln Lys Gly Gln Gln Ser Glu Ile
35 40 45
Asn Leu Lys Ile Pro Leu Val Ser Ala Ile Met Gln Ser Val Ser Gly
50 55 60
Glu Lys Met Ala Ile Ala Leu Ala Arg Glu Gly Gly Ile Ser Phe Ile
65 70 75 80
Phe Gly Ser Gln Ser Ile Glu Ser Gln Ala Ala Met Val His Ala Val
85 90 95
Lys Asn Phe Lys Ala Gly Phe Val Val Ser Asp Ser Asn Val Lys Pro
100 105 110
Asp Gln Thr Phe Ala Asp Val Leu Ala Ile Ser Gln Arg Thr Thr His
115 120 125
Asn Thr Val Ala Val Thr Asp Asp Gly Thr Pro His Gly Val Leu Leu
130 135 140
Gly Leu Val Thr Gln Arg Asp Tyr Pro Ile Asp Leu Thr Gln Thr Glu
145 150 155 160
Thr Lys Val Ser Asp Met Met Thr Pro Phe Ser Lys Leu Val Thr Ala
165 170 175
His Gln Asp Thr Lys Leu Ser Glu Ala Asn Lys Ile Ile Trp Glu Lys
180 185 190
Lys Leu Asn Ala Leu Pro Ile Ile Asp Asp Asp Gln His Leu Arg Tyr
195 200 205
Ile Val Phe Arg Lys Asp Tyr Asp Arg Ser Gln Val Cys His Asn Glu
210 215 220
Leu Val Asp Ser Gln Lys Arg Tyr Leu Val Gly Ala Gly Ile Asn Thr
225 230 235 240
Arg Asp Phe Arg Glu Arg Val Pro Ala Leu Val Glu Ala Gly Ala Asp
245 250 255
Val Leu Cys Ile Asp Ser Ser Asp Gly Phe Ser Glu Trp Gln Lys Ile
260 265 270
Thr Ile Gly Trp Ile Arg Glu Lys Tyr Gly Asp Lys Val Lys Val Gly
275 280 285
Ala Gly Asn Ile Val Asp Gly Glu Gly Phe Arg Tyr Leu Ala Asp Ala
290 295 300
Gly Ala Asp Phe Ile Lys Ile Gly Ile Gly Gly Ser Ile Xaa Ile
305 310 315 320
Thr Arg Glu Gln Lys Gly Ile Gly Arg Gly Gln Ala Thr Ala Val Ile
325 330 335
Asp Val Val Ala Glu Arg Asn Lys Tyr Phe Glu Glu Thr Gly Ile Tyr
340 345 350
Ile Pro Val Cys Ser Asp Gly Gly Ile Val Tyr Asp Tyr His Met Thr
355 360 365
Leu Ala Leu Ala Met Gly Ala Asp Phe Ile Met Leu Gly Arg Tyr Phe
370 375 380
Ala Arg Phe Glu Glu Ser Pro Thr Arg Lys Val Thr Ile Asn Gly Ser
385 390 395 400
Val Met Lys Glu Tyr Trp Gly Glu Gly Ser Ser Arg Ala Arg Asn Trp

405	410	415
Gln Arg Tyr Asp Leu Gly Gly Lys Gln	Lys Leu Ser Phe Glu Glu Gly	
420	425	430
Val Asp Ser Tyr Val Pro Tyr Ala Gly Lys Leu Lys Asp Asn Val Glu		
435	440	445
Ala Ser Leu Asn Lys Val Lys Ser Thr Met Cys Asn Cys Gly Ala Leu		
450	455	460
Thr Ile Pro Gln Leu Gln Ser Lys Ala Lys Ile Thr Leu Val Ser Ser		
465	470	475
Val Ser Ile Val Glu Gly Ala His Asp Val Ile Val Lys Asp Arg		
485	490	495
Ile Asn Asp Tyr His Pro Lys		
500		